TEAM 2

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/468,011*

DATE: 11/14/95
TIME: 16:05:12

INPUT SET: S7225.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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1                              SEQUENCE LISTING
2
3    (1)    General Information:
4
5         (i) APPLICANT: Soppet, Daniel R                   ENTERED
6                       Yi, Li
7                       Rosen, Craig A
8                       Ruben, Steven
9
10        (ii) TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
11               HLTDG74
12
13       (iii) NUMBER OF SEQUENCES: 8
14
15        (iv) CORRESPONDENCE ADDRESS:
16               (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
17                    Stewart & Olstein
18               (B) STREET: 6 Becker Farm Road
19               (C) CITY: Roseland
20               (D) STATE: NJ
21               (E) COUNTRY: USA
22               (F) ZIP: 07068-1739
23
24        (v) COMPUTER READABLE FORM:
25               (A) MEDIUM TYPE: Floppy disk
26               (B) COMPUTER: IBM PC compatible
27               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28               (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29
30        (vi) CURRENT APPLICATION DATA:
31               (A) APPLICATION NUMBER:  08/468,011
32               (B) FILING DATE: 06-JUN-1995
33               (C) CLASSIFICATION:
34
35      (viii) ATTORNEY/AGENT INFORMATION:
36               (A) NAME: Ferraro, Gregory D
37               (B) REGISTRATION NUMBER: 36,134
38               (C) REFERENCE/DOCKET NUMBER: 325800-458
39
40        (ix) TELECOMMUNICATION INFORMATION:
41               (A) TELEPHONE: 201-994-1700
42               (B) TELEFAX: 201-994-1744
43
44
45    (2) INFORMATION FOR SEQ ID NO:1:
46
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47        (i) SEQUENCE CHARACTERISTICS:
48             (A) LENGTH: 2003 base pairs
49             (B) TYPE: nucleic acid
50             (C) STRANDEDNESS: single
51             (D) TOPOLOGY: linear
52
53      (ii) MOLECULE TYPE: cDNA
54
55
56      (ix) FEATURE:
57             (A) NAME/KEY: CDS
58             (B) LOCATION: 90..1712
59
60
61      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
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63   GTTTGCTCTG GGCAGCCAAG TTGGCATATT GGAAGCTTTT TCCGGGCTCT GGAGGAGGGT        60
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65   CCCTGCTTCT TCCTACAGCC GTTCCGGGC ATG GCC TGG CTG GGG GCG TCG CTC        113
66                                    Met Ala Trp Leu Gly Ala Ser Leu
67                                     1               5
68
69   CAC GTC TGG GGT TGG CTA ATG CTC GGC AGC TGC CTC CTG GCC AGA GCC        161
70   His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala
71        10              15              20
72
73   CAG CTG GAT TCT GAT GGC ACC ATC ACT ATA GAG GAG CAG ATT GTC CTT        209
74   Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu
75    25              30              35              40
76
77   GTG CTG AAA GCG AAA GTA CAA TGT GAA CTC AAC ATC ACA GCT CAA CTC        257
78   Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu
79            45              50              55
80
81   CAG GAG GGA GAA GGT AAT TGT TTC CCT GAA TGG GAT GGA CTC ATT TGT        305
82   Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys
83            60              65              70
84
85   TGG CCC AGA GGA ACA GTG GGG AAA ATA TCG GCT GTT CCA TGC CCT CCT        353
86   Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro
87            75              80              85
88
89   TAT ATT TAT GAC TTC AAC CAT AAA GGA GTT GCT TTC CGA CAC TGT AAC        401
90   Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn
91        90              95              100
92
93   CCC AAT GGA ACA TGG GAT TTT ATG CAC AGC TTA AAT AAA ACA TGG GCC        449
94   Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala
95   105             110             115             120
96
97   AAT TAT TCA GAC TGC CTT CGC TTT CTG CAG CCA GAT ATC AGC ATA GGA        497
98   Asn Tyr Ser Asp Cys Leu Arg Phe Leu Gln Pro Asp Ile Ser Ile Gly
99        125             130             135
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102   Lys Gln Glu Phe Cys Glu Arg Leu Tyr Val Met Tyr Thr Val Gly Tyr
103            140                 145                 150
104
105   TCC ATC TCT TTT GGT TCC TTG GCT GTG GCT ATT CTC ATC ATT GGT TAC        593
106   Ser Ile Ser Phe Gly Ser Leu Ala Val Ala Ile Leu Ile Ile Gly Tyr
107            155                 160                 165
108
109   TTC AGA CGA TTG CAT TGC ACT AGG AAC TAT ATC CAC ATG CAC TTA TTT        641
110   Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe
111            170                 175                 180
112
113   GTG TCT TTC ATG CTG AGA GCT ACA AGC ATC TTT GTC AAA GAC AGA GTA        689
114   Val Ser Phe Met Leu Arg Ala Thr Ser Ile Phe Val Lys Asp Arg Val
115   185                 190                 195                 200
116
117   GTC CAT GCT CAC ATA GGA GTA AAG GAG CTG GAG TCC CTA ATA ATG CAG        737
118   Val His Ala His Ile Gly Val Lys Glu Leu Glu Ser Leu Ile Met Gln
119                      205                 210                 215
120
121   GAT GAC CCA CAA AAT TCC ATT GAG GCA ACT TCT GTG GAC AAA TCA CAA        785
122   Asp Asp Pro Gln Asn Ser Ile Glu Ala Thr Ser Val Asp Lys Ser Gln
123                220                 225                 230
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125   TAT ATC GGG TGC AAG ATT GCT GTT GTG ATG TTT ATT TAC TTC CTG GCT        833
126   Tyr Ile Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala
127            235                 240                 245
128
129   ACA AAT TAT TAT TGG ATC CTG GTG GAA GGT CTC TAC CTG CAT AAT CTC        881
130   Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu
131            250                 255                 260
132
133   ATC TTT GTG GCT TTC TTT TCG GAC ACC AAA TAC CTG TGG GGC TTC ATC        929
134   Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile
135   265                 270                 275                 280
136
137   TTG ATA GGC TGG GGG TTT CCA GCA GCA TTT GTT GCA GCA TGG GCT GTG        977
138   Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val
139                      285                 290                 295
140
141   GCA CGA GCA ACT CTG GCT GAT GCG AGG TGC TGG GAA CTT AGT GCT GGA       1025
142   Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly
143                300                 305                 310
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145   GAC ATC AAG TGG ATT TAT CAA GCA CCG ATC TTA GCA GCT ATT GGG CTG       1073
146   Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu
147            315                 320                 325
148
149   AAT TTT ATT CTG TTT CTG AAT ACG GTT AGA GTT CTA GCT ACC AAA ATC       1121
150   Asn Phe Ile Leu Phe Leu Asn Thr Val Arg Val Leu Ala Thr Lys Ile
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154   Trp Glu Thr Asn Ala Val Gly His Asp Thr Arg Lys Gln Tyr Arg Lys
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156

157   CTG GCC AAA TCG ACA CTG GTC CTG GTC CTA GTC TTT GGA GTG CAT TAC      1217
158   Leu Ala Lys Ser Thr Leu Val Leu Val Leu Val Phe Gly Val His Tyr
159               365             370             375
160

161   ATC GTG TTC GTG TGC CTG CCT CAC TCC TTC ACT GGG CTC GGG TGG GAG      1265
162   Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu
163             380             385             390
164

165   ATC CGC ATG CAC TGT GAG CTC TTC TTC AAC TCC TTT CAG GGT TTC TTT      1313
166   Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe
167             395             400             405
168

169   GTG TCT ATC ATC TAC TGC TAC TGC AAT GGA GAG GTT CAG GCA GAG GTG      1361
170   Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val
171       410             415             420
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173   AAG AAG ATG TGG AGT CGG TGG AAT CTC TCC GTG GAC TGG AAA AGG ACA      1409
174   Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr
175   425             430             435             440
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177   CCG CCA TGT GGC AGC CGC AGA TGC GGC TCA GTG CTC ACC ACC GTG ACG      1457
178   Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr
179               445             450             455
180

181   CAC AGC ACC AGC AGC CAG TCA CAG GTG GCG GCA GCA CAC GCA TGG TGC      1505
182   His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys
183             460             465             470
184

185   TTA TCT CTG GCA AAG CTG CCA AGA TCG CCA GCA GAC AGC CTG ACA GCC      1553
186   Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala
187             475             480             485
188

189   ACA TCA CTT TAC CTG GCT ATG TCT GGA GTA ACT CAG AGC AGG ACT GCC      1601
190   Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala
191       490             495             500
192

193   TCA CAC ACT CTC TCC ACG AGG AGC AAC AAG GAA GAT AGT GGG AGG CAG      1649
194   Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln
195   505             510             515             520
196

197   AGA GAT GAT ATT CTA ATG GAG AAG CCT TCC AGG CCT ATG GAA TCT AAC      1697
198   Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn
199               525             530             535
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201   CCA GAC ACT GAA GGA TGACAAGGAG AAACTGAGGA TGTTCTCTGA ATGGACATGT      1752
202   Pro Asp Thr Glu Gly
203               540
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205   GTGGCTGACT TTCATGGGCT GGTCCAATGG CTGGTTGTGT GAGAGGGCTT GGCTGATACT      1812
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207 CCTATGCTTG AGCACAAAGG CTGAAAATTC AGTTAAGGTG TTACTTAATA ATAGTTTTTA   1872
208
209 GGCTCCATGA ATTGGCTCCT GTAAATACTA ACGACATGAA AATGCAAGTG TCAATGGAGT   1932
210
211 AGTTTATTAC CTTCTATTGG CATCAAGTTT TCCTCTAAAT TAATGTATGG TATTTGCTCT   1992
212
213 GTGATTGTTC A   2003
214
215
216 (2) INFORMATION FOR SEQ ID NO:2:
217
218   (i) SEQUENCE CHARACTERISTICS:
219   (A) LENGTH: 541 amino acids
220   (B) TYPE: amino acid
221   (D) TOPOLOGY: linear
222
223   (ii) MOLECULE TYPE: protein
224
225   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
226
227 Met Ala Trp Leu Gly Ala Ser Leu His Val Trp Gly Trp Leu Met Leu
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230 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile
231   20   25   30
232
233 Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys
234   35   40   45
235
236 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe
237   50   55   60
238
239 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys
240   65   70   75   80
241
242 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys
243   85   90   95
244
245 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met
246   100   105   110
247
248 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe
249   115   120   125
250
251 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu
252   130   135   140
253
254 Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala
255 145   150   155   160
256
257 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg
258   165   170   175

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/468,011*

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